

Figure 11. Homology of *Drosophila how* (GadFly Accession Number CG10293) to human Quaking isoforms

Figure 11A. BLASTP results for CG10293 (GadFly Accession Number)

gb|AAF63416.1|AF142421_1 (AF142421) QUAKING isoform 5 [Homo sapiens]
Length = 337

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)
Query: SEQ ID NO: 23; Sbjct: SEQ ID NO: 24

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
P A P PLI + V + PTAA G G+I+ PY+Y Y
Sbjct: 240 PTPAGPTIMPLIRQIQTA-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 292

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
+L + S +GA+ + R R HPYQR
Sbjct: 293 ATSILEYPIEPSGVLGAVATKVRRHDMRVHPYQR 326

ref|XP_037438.2| (XM_037438) similar to KH domain RNA binding protein QKI-5A
[Homo sapiens], Length = 341

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)
Query: SEQ ID NO: 23; Sbjct: SEQ ID NO: 25

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 126 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
 P A P PLI + V + + PTAA G G+I+ PY+Y Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 296

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
 +L + S +GA+ + R R HPYQR
 Sbjct: 297 ATSILEYPIEPSGVLGAVATKVRRHDMRVHPYQR 330

gb|AAF63414.1|AF142419_1 (AF142419) QUAKING isoform 6 [Homo sapiens]
 Length = 363

Score = 289 bits (739), Expect = 5e-77
 Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)
 Query: SEQ ID NO: 23; Sbjct: SEQ ID NO: 26

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 88 EKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAE 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 265

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
 P A P PLI + V + + PTAA G G+I+ PY+Y Y
 Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 318

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
 +L + S +GA+ + R R HPYQR
 Sbjct: 319 ATSILEYPIEPSGVLGAVATKVRRHDMRVHPYQR 352

dbj|BAB55032.1| (AK027309) unnamed protein product [Homo sapiens]
 Length = 323

Score = 282 bits (722), Expect = 5e-75
 Identities = 165/320 (51%), Positives = 208/320 (64%), Gaps = 20/320 (6%)
 Query: SEQ ID NO: 27; Sbjct: SEQ ID NO: 28

Query: 81 QLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-VKKEPLTLPEPEGSV 134
 QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+ G +
 Sbjct: 2 QLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGSTEKRSaelPDAVGPI 61

Query: 135 VTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKEDANR 194
 V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE+ NR
 Sbjct: 62 VQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKEQNR 121

Query: 195 GKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEGEDELKKRQLMELAI 254
 GKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLMELAI
 Sbjct: 122 GKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEGEDSLKKMQLMELAI 181

Query: 255 INGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAPLIILN 313
 +NGTYRD KS A+ A + R++T A +R P A P PLI
 Sbjct: 182 LNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRTPTPAGPTIMPLIRQ 239

Query: 314 PRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALAGNPLLTEYADHS-- 369
 + V + + PTAA G G+I+ PY+Y Y +L + S
 Sbjct: 240 IQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAPATSILEYPIEPSGV 292

Query: 370 VGAIKQQRRLATNREHPYQR 389
 +GA+ + R R HPYQR
 Sbjct: 293 LGAVATKVRRHDMRVHPYQR 312

gb|AAF63413.1|AF142418_1 (AF142418) QUAKING isoform 2 [Homo sapiens]
 Length = 347

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 30

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVKMDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 88 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAILNGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRT 265

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63417.1|AF142422_1 (AF142422) QUAKING isoform 3 [Homo sapiens]
 Length = 341

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 31

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVKMDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 88 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRRRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPALRT 265

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 266 PTPAGPTIMPLIRQIQTA V-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63415.1|AF142420_1 (AF142420) QUAKING isoform 4 [Homo sapiens]
 Length = 315

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 32

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 122 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRRRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPALRT 239

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 240 PTPAGPTIMPLIRQIQTA V-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BAB69497.1| (AB067799) RNA binding protein HQK-6 [Homo sapiens]
 Length = 319

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 33

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRRRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPALRT 243

22/51

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTA-----MPNGTPHPTAAIVPPGPEAGLIYTPY 290

dbj|BAB69499.1| (AB067801) RNA binding protein HQK-7B [Homo sapiens]
 Length = 319

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 34
 Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65
 Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125
 Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQKLLVPPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAG 185
 Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 243
 Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTA-----MPNGTPHPTAAIVPPGPEAGLIYTPY 290

dbj|BAB69498.1| (AB067800) RNA binding protein HQK-7 [Homo sapiens]
 Length = 325

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 35
 Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65
 Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125
 Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQKLLVPPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAG 185
 Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 243
 Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTA-----MPNGTPHPTAAIVPPGPEAGLIYTPY 290

gb|AAF63412.1|AF142417_1 (AF142417) QUAKING isoform 1 [Homo sapiens]
Length = 321

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)
Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 36

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKMLSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSaelPDavgPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEaETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAevQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRaeIKLKRAVEEVKLLVPAaEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDslKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPpAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAafdQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BD004960.1| Genes related to stomach cancer, Length = 1993

Score = 288 bits (738), Expect = 1e-77
Identities = 168/324 (51%), Positives = 211/324 (64%), Gaps = 11/324 (3%)
Frame = +1
Query: SEQ ID NO: 37; Sbjct: SEQ ID NO: 38

Query: 77 DYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-VKKEPLTLPEP 130
DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+
Sbjct: 4 DYLMQLMNDKMLSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGSTeKRSaelPDa 183

Query: 131 EGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKE 190
G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE
Sbjct: 184 VGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEaETGCKIMVRGKGSMRDKKKE 363

Query: 191 DANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAevQKLLVPQAEGeDELKKRQLM 250
+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLM
Sbjct: 364 EQNRGKPNWEHLNEDLHVLITVEDAQNRaeIKLKRAVEEVKLLVPAaEGEDslKKMQLM 543

Query: 251 ELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAP 309
ELAI+NGTYRD KS A+ A + R++T A +R P A P P
Sbjct: 544 ELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPpAALRTPTPAGPTIMP 717

Query: 310 LILNPRMTVPTTAASILSAQAAPTAafdQTG--HGMIFAPYDYANYAALAGNPLLTEYAD 367
LI + V + + PTAA G G+I+ PY+Y Y +L +
Sbjct: 718 LIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAPATSILEYPIE 876

Query: 368 HS--VGAIKQQRRLATNREHPYQR 389
S +GA+ + R R HPYQR
Sbjct: 877 PSGVLGAVATKVRRHDMRVHPYQR

Figure 15. Homology of Drosopila GadFly Accession Number CG9373 to human KIAA1443 protein, human unnamed protein product, and human myelin gene expression factor 2

**Figure 15A. BLASTP results for GadFly Accession Number CG9373
Homology to human protein BAA92579.1 (GenBank Accession Number)**

dbj|BAA92579.1| (AB037762) KIAA1341 protein [Homo sapiens], Length = 620

Score = 249 bits (635), Expect = 1e-64

Identities = 207/660 (31%), Positives = 295/660 (44%), Gaps = 148/660 (22%)

Query: SEQ ID NO: 44; Sbjct: SEQ ID NO: 45

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Query: 1  MSMDASNSVESREKERDRRGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
      + M+  S + + + + G++ +RF      + N G G + G      RN R
Sbjct: 72  VKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 121

Query: 59  VYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDES GKARGCGIVEFKDPENVQKALEKM 118
      V+ISNIPYD+WQ +KDL R  VG + YV+LF D  GK+RCCG+VEFKD E V+KALE M
Sbjct: 122  VFISNIPYDMKWQAIDLMREKVGEVTVYVELFKDAEGKSRGCGVVEFKDEEFVKKALETM 181

Query: 119  NRYEVNGRELVVKEDHGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNNGGGGGGGGRDHMD 178
      N+Y+++GR L +KED  + +  + R GG  GG      H+
Sbjct: 182  NKYDLSGRPLNIKEDPDGENARRA-LQRTGGSFPGG-----HVP 219

Query: 179  DRDRGFSSRDDRRLSGRNNFNMMSSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVAN 238
      D  G      L  NN N+  +N      +G L + +FVAN
Sbjct: 220  DMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVAN 259

Query: 239  LDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISM LDRQMLF 298
      LD+KV  KKLK+VF +AG V+  D+  DK+G SRG  + ++  +EAVQAISM + Q LF
Sbjct: 260  LDFKVGWKKLKEVFSSIAGTVKRA DIKEDKDGKSRGMGTVTTFEQAIEAVQAISMFGNQFLF 319

Query: 299  DRRM TVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNLPNGGQSQ 350
      DR M V++D  +P +      + +LP GLGG+G+GLGP G+P+  N+
Sbjct: 320  DRPMHVKMDDKSVPH EYRSHDGKTPQLPRGLGGIGMGLGPGGQPISASQLNI----- 372

Query: 351  GQLLGNAQQGSQLGSGVGSQPNSSAVSNATTNLLNNLTGVMFGNHA AVQPSVPAPVQKPSL 410
      G ++GN  G      + G FG      +
Sbjct: 373  GGVMGNLGP GGM-----GMDGPGFGG-----MNRI 397

Query: 411  GNNTGSGGLNLLNNLNPSILAAVVGNLGNQG--GNLSNPLLSSSL-----SNLGLNLGNS 462
      G  G GGL  N      +G G G G L  ++SS+  ++G+N G
Sbjct: 398  GGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRGFG 449

Query: 463  GNDDNLPPSNVGLSNNYSSGGTGGGNSYSSGNNYSGGGGSSN-----LGYNAYSSS-G 514
      +  L + +G      +G G N  G+  SGG GS N      +G +  SSS
Sbjct: 450  DSFGRLGSAMIG----GFAGRIGSSNMGPVSGISGGMGSMNSVTGGMGMLDRMSSSFD 505

Query: 515  GMGGGNGGVGVDGNDYNTGNPLDVYGGGNSVGNNSVGSANAVGASRKSDTIIIKNPVITC 574
      MG G G +  D + G      G G      +GS      K + I ++N+P
Sbjct: 506  RMGPGIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDL 554

Query: 575  TWQTLRDKFREIGDVKFAEI-----RGNDVGVRFFKERRDAELALALMDGSRLDGRNIKV 629
      TWQ L++KF + G V FAEI      +  G VRF      AE A  +M+G ++ GR I V
Sbjct: 555  TWQKLKEKFSQCCHVMPAEIKMENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDV 614

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Score = 68.6 bits (166), Expect = 2e-10
 Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)
 Query: SEQ ID NO: 46; Sbjct: SEQ ID NO: 47
 Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79
 G GA R D D G +G G G+ R+R + N ++++ N+P+D WQ LK+ F +
 Sbjct: 510 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 565
 Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYEVNGRELVVKED 133
 G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
 Sbjct: 566 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLD 617

Score = 56.2 bits (134), Expect = 1e-06
 Identities = 46/180 (25%), Positives = 76/180 (41%), Gaps = 21/180 (11%)
 Query: SEQ ID NO: 48; Sbjct: SEQ ID NO: 49
 Query: 139 DQYGRIVRDGGGGGGG-----GGGVQGGNGGNGGGGGGGGRDHMDRDRGFSRRD 188
 D +GR+ GG G G G+ GG G N GG G +D F R
 Sbjct: 450 DSFGRLGSAMIGGFAGRIGSSNMGPVGSIGSGMGSMSVTGGMGMG-LDRMSSSFDRM- 507
 Query: 189 DDRLSGRNNFNMSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVANLDYKVDNKKL 248
 G ++ + + + + E +G G N++FV NL + + +KL
 Sbjct: 508 -----GPGIGAILERSIDMDRGFLSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKL 559
 Query: 249 KQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
 K+ F G V ++ ++ G S+G + +D P A +A +++ + R + VRLDR
 Sbjct: 560 KEKFSQCGHVMFAEIKMEN-GKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDR 618

Homology to human protein BAB14421.1 (GenBank Accession Number)

>dbj|BAB14421.1| (AK023133) unnamed protein product [Homo sapiens],
 Length = 576

Score = 242 bits (618), Expect = 1e-62
 Identities = 206/654 (31%), Positives = 289/654 (43%), Gaps = 160/654 (24%)
 Query: SEQ ID NO: 44; Sbjct: SEQ ID NO: 50
 Query: 1 MSMDASNSVESREKERDRRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
 + M+ S + + + + G++ +RF + N G G + G RN R
 Sbjct: 52 VKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 101
 Query: 59 VYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKM 118
 V+ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE M
 Sbjct: 102 VFISNIPYDMKWQAIKDLMEKVG EYTYVELFKDAEGKSRGCGVVEFKDEEFVKKALETM 161
 Query: 119 NRYEVNGRELVVKED-HGEQRDQYGRIVRDGGGGGGGGGGGVQGGNGGNGGGGGGGGRDH 177
 N+Y+++GR L +KED GE + + R GG GG H+
 Sbjct: 162 NKYDLSGRPLNIKEDPDGENARRASQ--RTGGSFPGG-----HV 198
 Query: 178 DDRDRGFSRRDDRLSGRNNFNMSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVA 237
 D G L NN N+ +N +G L + +FVA
 Sbjct: 199 PDMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVA 238
 Query: 238 NLDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQML 297
 NLD+KV KKLK+VF +AG V+ D+ DK+G SRG + ++ +EAVQAISM + Q L
 Sbjct: 239 NLDKFKVGWKKLKEVFSIAGTVKRADIKEDKDGKSRGMGTVTFEQAIEAVQAISMFGQFL 298
 Query: 298 FDRRMTVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNLPNGGQS 349

Sbjct: 299 FDR M V++D +P + + +LP GLGG+G+GLGP G+P+ N+
 Query: 350 QGQLLGNAQQGSQGLSVGSQPNSSAVSNATTNLLNNLTGVMFGNHAAVQSPFVAPVQKPS 409
 G ++GN G + G FG
 Sbjct: 353 -GGVMGNLGP GGM-----GMDGPGFGG-----MNR 376
 Query: 410 LGNNTGSGGLNLLNNLNP SILAAVGNLGNQG--GNLSNPLLSSSL-----SNLGLNLGN 461
 +G G GGL N +G G G G L ++SS+ ++G+N G
 Sbjct: 377 IGGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRG- 427
 Query: 462 SGNDNLPPSNVGLSNYSSGGTGGGNSYSSGNYSGGGGSSNLGYNAYSSS-GGMGGGN 520
 G S GG GG NS + G +G + SSS MG G
 Sbjct: 428 -----FGDSFGRLGGGMGGMNSVT-----GGMGMGLDRMSSSFDRMGPGI 467
 Query: 521 GGVGVDGNDYNTGNPLDVYGGGNSVGNVGSANAVGASRKSDTIIKKNVPITCTWQTLR 580
 G + D + G G G +GS K + I ++N+P TWQ L+
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLFPDLTWQKLK 516
 Query: 581 DKFREIGDVKFAEI-----RGNDVGVRFFKERDAELAIALMDGSRLDGRNIKV 629
 +KF + G V FAEI + G VRF AE A +M+G ++ GR I V
 Sbjct: 517 EKFSQCGHVMFAEIKMENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDV 570

Score = 72.8 bits (177), Expect = 1e-11

Identities = 82/348 (23%), Positives = 133/348 (37%), Gaps = 96/348 (27%)

Query: SEQ ID NO: 51; Sbjct: SEQ ID NO: 52

Query: 54 RRNCRVYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQK 113
 R ++++N+ + W+ LK++F I G+++ + D+ GK+RG G V F+ +
 Sbjct: 230 RLGSTIFVANLDFKVGWKKLKEVFS-IAGTVKRA DIKEDKD GKS RGMGTVTTFEQAI EAVQ 288
 Query: 114 ALEKMNRYE VNGREL VVKED-----HGEQRDQYGRIVRDGGGGGGGG----- 155
 A+ N + R + VK D H E R G+ + G GG G
 Sbjct: 289 AISMFNGQFLFDRPMHVKMDDKSVPH E EYRSHD G K T P Q L P R G L G G I G M G L G P G G Q P I S A S 348
 Query: 156 ----GGVQG-----GNGGNNGGGGG-----GGRDHMDRDRDRGF 184
 GGV G G GG N GGG GG M + RG
 Sbjct: 349 QLNIGGVGMGNLGP GGMGMDGPGFGGMNRIGGGIGFGGLEAMNSMGGFGGVGRMGELYRGA 408
 Query: 185 SRRDDRLSGRNNFNMM-----NDYNNSSNYNLYGLSASFLES LG--- 225
 +R GR + + N L +S+SF + +G
 Sbjct: 409 MTSSMERDFGRGDIGINRGFGDSFGRLGGGMGGMNSVTGGMGMGLDRMSSSF-DRMGPGI 467
 Query: 226 -----ISGPLH-----NKVFVANLDYKVDNKKLQVFKLAGKVQS 260
 +SGP+ N++FV NL + + +KLK+ F G V
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGMRERIGSKGNQIFVRNLFPDLTWQKLKEKFSQCGHVMF 527
 Query: 261 VDLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
 ++ ++ G S+G + +D P A +A +++ + R + VRLDR
 Sbjct: 528 AEIKMEN-GKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLDR 574

Score = 68.6 bits (166), Expect = 2e-10

Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: SEQ ID NO: 46; Sbjct: SEQ ID NO: 53

Query: 20 GRGARGSRFTDADGNGAGSQGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79
 G GA R D D G +G G G+ R+R + N ++++ N+P+D WQ LK+ F +
 Sbjct: 466 GIGAILERSIDMD-RGFLSGPMGSGM---RERIGSKGN-QIFVRNLFPDLTWQKLKEKFSQ 521
 Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYE VNGREL VVKED 133

G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
Sbjct: 522 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLD 573

Homology to human protein NP057216.1 (GenBank Accession Number)

ref|NP_057216.1| (NM_016132) myelin gene expression factor 2 [Homo sapiens]
gb|AAD43038.1| (AF106685) myelin gene expression factor 2 [Homo sapiens]
Length = 547

Score = 238 bits (607), Expect = 2e-61
Identities = 204/659 (30%), Positives = 295/659 (43%), Gaps = 150/659 (22%)
Query: SEQ ID NO: 54; Sbjct: SEQ ID NO: 55

Query: 3 MDASNSVESREKERDRRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCRVY 60
M+ S + + + + G++ +RF + N G G + G RN RV+
Sbjct: 1 MENDESAKEEKSDDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-RVF 50

Query: 61 ISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDES GKARGCGIVEFKDPENVQKALEKMN 120
ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGG+VEFKD E V+KALE MN+
Sbjct: 51 ISNIPYDMKWQAIKDLMREKVGEVTVYVELFKDAEGKSRGCGVVEFKDEEFVKALETMNK 110

Query: 121 YEYVNGRELVVKEDHGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNGGGGGGGGRDHMD 180
Y+++GR + +KED + + + R G QG + + G G
Sbjct: 111 YDLSGRRVNIKEDPDGENARRA-LQRTGTS-----FQGS HASDVGSG----- 151

Query: 181 DRGFSRRDDRLSGRNNFMMSNDYMNSSNYNLYGLSASFLES LGISGPLHNKVFVANLD 240
N+ + NN + + + +L +G L + +FVANLD
Sbjct: 152 -----LVNLPSPILNNPN-----IPPEVISNLQ-AGRLGSTIFVANLD 188

Query: 241 YKVDNKKLKQVFKLAGKVQSVDSL DKEGNSRGFAVIEYDHPVEAVQAI SMLDRQMLFDR 300
+KV KKLK+VF +AG V++ DK+G SRG + ++ +EAVQAISM + Q LFDR
Sbjct: 189 FKGWKKLKEVFSIAGTVKAGSYKEDKD GKS RGMGTVTTFEQAI EAVQAISM FNGQFLFDR 248

Query: 301 RMTVRLD-----RIPDKNEG IKLPEGLGGVGIGLGPNGEPLRDVAHNL PNGGQSQG 351
M V++D R PD + +LP GLGG+G+GLGP G+P+ N+ G
Sbjct: 249 PMHVKMDKSPHEEYRSPD-GKTPQLPRGLGGIGMGLPGGPQIPISASQLNI-----G 300

Query: 352 QLLGNAQQGSQSGSVGSQPNSSAVSNATTNLLNNLTGVMFGNHA AVQSPVPVQKPSLG 411
++GN G + G FG +G
Sbjct: 301 GVMGNLGP GGM-----GMDGPGFGG-----MNRIG 325

Query: 412 NNTGSGGLNLLNNLNPSILAAVVG NLGNQG--GNLSNPLLSSSL S-----NLGLNLGNSG 463
G GGL N +G G G G L ++SS+ ++GL+ G
Sbjct: 326 GGIGFGGLEAMN-----SMGGFGGVGRMGEL YRGAMTSSMERDFGHRDIGLSRGFGD 377

Query: 464 NDDNLPPSNVGLSNNYSSGGTGGGNSYSSGNYS SGGGSSN-----LGYNAYSSS-GG 515
+ L + +G +G G N G+ SGG GS N +G + SSS
Sbjct: 378 SFGR LGSAMIG----GITGRIGSSNMGPVGS GISGGMGSMNSVTGGMGMLDRMSSSFDR 433

Query: 516 MGGGNGGVGVDGNDYNTGNPLDVYGGGNSVGNNSVGSANAVGASRKSDTII IKNVPITCT 575
MG G G + D + G G G +GS K + I ++N+P T
Sbjct: 434 MGPGIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDLT 482

Query: 576 WQTLRDKFREIGDVKFAEI-----RGNDVG VVRFFKERDAELALMDGSRLDGRNIKV 629
WQ L++KF + G V FAEI + G VRF AE A +M+G ++ GR I V
Sbjct: 483 WQKLKEKFSQCGHVMFAEIKMENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDV 541

Score = 68.6 bits (166), Expect = 2e-10

Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: SEQ ID NO: 46; Sbjct: SEQ ID NO: 56

Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79

G GA R D D G +G G G+ R+R + N ++++ N+P+D WQ LK+ F +

Sbjct: 437 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 492

Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYEVNGRELIVVKED 133

G + + + + E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D

Sbjct: 493 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDVRLD 544

Score = 55.5 bits (132), Expect = 2e-06

Identities = 41/157 (26%), Positives = 69/157 (43%), Gaps = 11/157 (7%)

Query: SEQ ID NO: 57; Sbjct: SEQ ID NO: 58

Query: 152 GGGGGGVQGGNGGNGGGGGGGGRDHMDRDRGFSRRDDRLSGRNNFNMMNSNDYNNSSNY 211

G G G+ GG G N GG G +D F R G ++ + +

Sbjct: 400 GPVGSGISGGMGSMNSVTGGMGMG-LDRMSSSFDRM-----GPGIGAILERSIDMDRGF 452

Query: 212 NLYGLSASFLESGLISGPLHNKVFFVANLDYKVDNKKLKQVFKLAGKVQSVDLSDKEGNS 271

+ + E +G G N++FV NL + + +KLK+ F G V ++ ++ G S

Sbjct: 453 LSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKLKEKFSQCGHVMFAEIKMEN-GKS 508

Query: 272 RGFVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308

+G + +D P A +A +++ + R + VRLDR

Sbjct: 509 KGCGTVRFDSPEAEKACRIMNGIKISGREIDVRLDR 545

Figure 15B. Multiple Sequence Alignment (ClustalW 1.83)

CG9373 Dm -----
KIAA1341 Hs PLSRSEPLSSGGRGGGSGGGMADANKAEVPGATGGDSPHLQPAEPPGEPRREPHPAEAEK
MyEF-2 Hs -----
FLJ13071 Hs -----MADANKAEVPGATGGDSPHLQPAEPPGEPRREPHPAEAEK

CG9373 Dm ---MSMDASNSVESREKERDRRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNC
KIAA1341 Hs QQPQHSSSSNGVKMENDESAKEEKS DLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNNRN
MyEF-2 Hs -----MENDESAKEEKS DLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNNRN
FLJ13071 Hs QQPQHSSSSNGVKMENDESAKEEKS DLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNNRN

CG9373 Dm RYVYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEK
KIAA1341 Hs RVFISNIPYDMKWQA IKDLMREKVG EYTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET
MyEF-2 Hs RVFISNIPYDMKWQA IKDLMREKVG EYTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET
FLJ13071 Hs RVFISNIPYDMKWQA IKDLMREKVG EYTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET

CG9373 Dm MNRYEVNGRELIVVKEDHGEQRDQYGRIVRDGGGGGGGGGGGVQGGNGGNGGGGGGGGRDHM
KIAA1341 Hs MNKYDLSGRPLNIKEDPDGENARR-----ALQRTGGSFPGGHVPDMGSG-----
MyEF-2 Hs MNKYDLSGRRVNIKEDPDGENARR-----ALQRTGTSFQGS HASDVGSG-----
FLJ13071 Hs MNKYDLSGRPLNIKEDPDGENARR-----ASQRTGGSFPGGHVPDMGSG-----

CG9373 Dm DDDRDRGFSRRDDRLSGRNNFNMMNSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFA
KIAA1341 Hs -----LMNLPPSILNPNIPPEVISNLQ----AGRLGSTIFVA
MyEF-2 Hs -----LVNLPPSILNPNIPPEVISNLQ----AGRLGSTIFVA
FLJ13071 Hs -----LMNLPPSILNPNIPPEVISNLQ----AGRLGSTIFVA